



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/729,340
Source: FFWD-
Date Processed by STIC: 12/18/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA. 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 101729,340
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. <u>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</u>	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/729,340

DATE: 12/18/2003

TIME: 08:56:41

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

1 <110> APPLICANT: Jager, Dirk
 2 Stockert, Elizabeth
 3 Scanlan, Matthew
 4 Gure, Ali
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
 Antigens,
 10 the Antigens Per Se, and Uses Thereof
 12 <130> FILE REFERENCE: LUD 5793.1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/729,340
 C--> 15 <141> CURRENT FILING DATE: 2003-12-04
 17 <150> PRIOR APPLICATION NUMBER: US 09/451,739
 18 <151> PRIOR FILING DATE: 2000-06-22
 W--> 20 <150> PRIOR APPLICATION NO: US 09/451,739
 21 <151> PRIOR FILING DATE: 1999-11-30
 23 <160> NUMBER OF SEQ ID NOS: 32

Does Not Comply
 Corrected Diskette Needed
 (pg. 1,2,3,4,7,9-11)

ERRORED SEQUENCES

245 <210> SEQ ID NO: 8
 246 <211> LENGTH: 772
 247 <212> TYPE: DNA
 248 <213> ORGANISM: Homo sapiens
 249 <221> NAME/KEY: CDS
 250 <222> LOCATION: 695-714
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 252 aaagcgttct cggcgggagc gcaacaacta gaaccgtgag aacgcgtcca gcaaccgcga 60
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 254 agcagggtc catggccaag gctagcggc aggcgtcccc cgcagacctc cccatcgacc 180
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 256 tccgcttctc gtgtgtgagt ctcaaccata aaccaaagcg caagtggtag tgttccagat 300
 257 gcgggggaaa gacgatggg caaagccctt gagaagtcca gaaaaaaaac agggcttata 360
 258 acaggtagtt tggggacatg cgtctaatag tgaggagaac aaaataagcc agtgtgttga 420
 259 ttacattgca acctttgctg aggtgcagga agtgtaaaat gtatatTTTT aaagaatgtt 480
 260 gttagggggt gggcgcggtg gctcacgctt gtaatcccag cactttggga ggccgagggc 540
 261 gtccgctac gaggtcagga gatcgagacc atcctggcta acacggtgaa accccgtctc 600
 262 tactaataat tcaaaaaaaaa aattagctgg gctgggtggc gggcgctgt agtcccagct 660
 W--> 263 attcggagg ctgaggcagg agaattgggt gaactggga ggtggagctt gcantgagcc 720
 264 aaggtcgcgc cactgcactc cagcctgggt gacagagcga gactccatct ta 772
 315 <210> SEQ ID NO: 15
 316 <211> LENGTH: 2030

There is a CDS
 at this location.

insert this mandatory
 numeric identifier
 whenever <221>
 <222> or <223>
 is shown.

<220> <223> - please insert to explain N locations. see 1.823

Sequence Rules

please see error summary sheet.

RAW SEQUENCE LISTING

DATE: 12/18/2003

PATENT APPLICATION: US/10/729,340

TIME: 08:56:41

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

317 <212> TYPE: DNA

318 <213> ORGANISM: Homo sapiens

319 <221> NAME/KEY: CDS

320 <222> LOCATION: 1628, 1752, 1758, 1769, 1789, 1873, 1908, 1915, 1933, 1970, 1976,

2022

<223>

OK

321 <400> SEQUENCE: 151

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 323 ctaaagcctt agaattgatg gacatgcaaa ctttcaaagc agagcctccc gagaagccat 120
 324 ctgccttcga gacctgccatt gaaatgcaaa agtctgttcc aaataaagcc ttggaattga 180
 325 agaatgaaca aacattgaga gcagatgaga tactcccatc agaatccaaa caaaaggact 240
 326 atgaagaaag ttcttgggat tctgagagtc tctgtgagac tgtttcacag aaggatgtgt 300
 327 gtttacccaa ggctacacat caaaaagaaa tagataaaat aaatggaaaa ttagaagagt 360
 328 ctctgataa tgatggtttt ctgaaggctc cctgcagaat gaaagtcttct attccaacta 420
 329 aagccttaga attgatggac atgcaaacct tcaaagcaga gcctcccgag aagccatctg 480
 330 ccttcagacc tgccattgaa atgcaaaagt ctgttccaaa taaagccttg gaattgaaga 540
 331 atgaacaaac attgagagca gatcagatgt tcccttcaga atcaaaacaa aagaaggttg 600
 332 aagaaaattc ttgggattct gagagtctcc gtgagactgt ttcacagaag gatgtgtgtg 660
 333 taccacaggc tacacatcaa aaagaaatgg ataaaataag tggaaaatta gaagattcaa 720
 334 ctagcctatc aaaaatcttg gatacagttc attcttgtga aagagcaagg gaacttcaaa 780
 335 aagatcactg tgaacaacgt acaggaaaaa tggaaacaaat gaaaaagaag ttttgtgtac 840
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 337 aatgggaaca agagctctgc agtgtgagat tgactttaaa ccaagaagaa gagaagagaa 960
 338 gaaatgccga tatattaaat gaaaaaatta gggagaagatt aggaagaatc gaagagcagc 1020
 339 ataggaaaga gttagaagtg aaacaacaac ttgaacaggc tctcagaata caagatatag 1080
 340 aattgaagag ttagaagaagt aatttgaatc aggtttctca cactcatgaa aatgaaaatt 1140
 341 atctcttaca tgaaaattgc atgttgaaaa aggaaattgc catgctaaaa ctggaaatag 1200
 342 ccacactgaa acaccaatac caggaaaaagg aaaataaata ctttgaggac attagattt 1260
 343 taaaagaaaa gaatgctgaa cttcagatga ccctaaaact gaaagaggaa tcattaacta 1320
 344 aaagggcatc tcaatatagt gggcagctta aggttctgat agctgagaac acaatgctca 1380
 345 cttctaaatt gaaggaaaaa caagacaaag aaataactaga ggcagaaatt gaatcacacc 1440
 346 atcctagact ggtcttctgt gtacaagacc atgatcaaat tgtgacatca agaaaaagtc 1500
 347 aagaacctgc tttccacatt gcaggagatg cttgtttgca aagaaaaatg aatgttgatg 1560
 348 tgagtagtac cgatatataa caatgaggtg ctccatcaac cactttctga agctcaaagg 1620
 349 aaatccaaa gcctaaaaat taatctcaat tatgcaggag atgtctctaa agaaaataca 1680
 350 ttggtttcag gaacatgcac aaagagacca acgtgaaaca cagtgtcaaa tgaaggagc 1740
 351 tgaacacatg ttcaaaacg aacaagatga tgtgaacaaa cacactgaac agcaggagtc 1800
 352 tctagatcag aaattatttc aactacaaag caaaaatatg tggcttcaac agcaattagt 1860
 353 tcatgcacat aatgaaagct gacaacaaaa gcaagataac aattgatatt catttcttg 1920
 354 agaggaaaat gacatcatc ttctaaaaga gaaaaatgag gagatatttt attacataa 1980
 355 ccatttataa aaccctgata tttcaatatg gaaaaaaaaa anaaaaaaaa 2030

358 <210> SEQ ID NO: 16

359 <211> LENGTH: 513 512 shown

360 <212> TYPE: PRT

361 <213> ORGANISM: Homo sapiens

W-->

362 <400> SEQUENCE: 16

363 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
 364 1 5 10 15
 365 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 366 20 25 30
 367 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn

SAME errors
 see error summary
 sheet.

Please
 see error
 summary
 sheet regarding
 the use of ns/Kaas.

RAW SEQUENCE LISTING

DATE: 12/18/2003

PATENT APPLICATION: US/10/729,340

TIME: 08:56:41

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

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369 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
370          50          55          60
371 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
372 65          70          75          80
373 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
374          85          90          95
375 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
376          100         105         110
377 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
378          115         120         125
379 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
380          130         135         140
381 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
382 145          150         155         160
383 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
384          165         170         175
385 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
386          180         185         190
387 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
388          195         200         205
389 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
390          210         215         220
391 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
392 225          230         235         240
393 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
394          245         250         255
395 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
396          260         265         270
397 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
398          275         280         285
399 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
400          290         295         300
401 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
402 305          310         315         320
403 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
404          325         330         335
405 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
406          340         345         350
407 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 408 (325) 355          360          365
409 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
410          370         375         380
411 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
412 385          390         395         400
413 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
414          405         410         415
415 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
416          420         425         430

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DATE: 12/18/2003

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

417 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
 418 435 440 445
 419 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
 420 450 455 460
 421 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
 422 465 470 475 480
 423 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
 424 485 490 495
 425 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
 426 500 505 510
 773 <210> SEQ ID NO: 26.
 774 <211> LENGTH: 3673
 775 <212> TYPE: DNA
 776 <213> ORGANISM: Homo sapiens
 777 <221> NAME/KEY: CDS/
 778 <222> LOCATION: 439, 473, 1789
 779 <400> SEQUENCE: 26
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 781 gggcgagtgc gagccggggg cgggtgctgg ggaagggtaa gcgggaagcg agggcgaggg 120
 782 gtaggggctg gggaagggcg agcgggaggg cggggtcttc tctagcaggg ggctgcagcc 180
 783 atgaagaggc tcttagctgc cgctggcaag ggcgtgcggg gcccgagacc cccgaacccc 240
 784 ttcagcgaac ggggtctacac tgagaaggac tacgggacca tctacttcgg gatctaggg 300
 785 aagatccata cagctgcctc ccggggccaa gtccagaagc tggagaagat gacagtaggg 360
 786 aagaagcccg tcaacctgaa caaaagagat atgaagaaga ggactgctct acactggggc 420
 787 ~~tgtgtcaatg gccatgcana agtagtaaca tttctggtag acagaaagtg cctgcttaat~~ 480
 788 gtccttgatg gogaagggag gacacctctg atgaaggctc tacaatgcga gagggaaagt 540
 789 ttgtgcaaat attctcatag atgctggtgc tgatctaaat tatgtagatg tgtatggcaa 600
 790 cacggtcttc cattatgccg tttatagtga gaatttatta atggtggcaa cactgctgtc 660
 791 ctatggtgca gtcacagagg tgcaaaacaa ggctagcctc acacccttt tactggccat 720
 792 acagaaaaga agcaagcaaa ctgtggaatt ttactaaca aaaaatgcaa atgcaaagcg 780
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 795 tgcagaacgt tatgctgctg ctgctggagt taattacatt catcaacaac ttttggaaac 960
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 798 aaaaacacct gacgaggctg cacgcttggg ggagggaacg tctgcaaaa ttcaatgtct 1140
 799 ggggaaagca acatctggaa agtttgaaca gtcaacagaa gaaacacctt ggaaaatttt 1200
 800 gaggcctaca aaagaaacat ctgagaaatt ttcattggca gcaaaagaaa gatctaggaa 1260
 801 gatcacatgg gaggaaaaag aaacatctgt aaagactgaa tgcgtggcag gagtaacacc 1320
 802 taataaaact gaagttttgg aaaaaggaac atctaatatg attgcatgtc ctacaaaaga 1380
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 804 ttttggcaca cggactattg aaaattcaca gtgtacaaaa gttgaggaag actttaatct 1500
 805 tgctaccaag attatctcta agagtgtctc acagaattat acgtgtttac ctgatgtctac 1560
 806 atatcaaaaa gatatacaaa caataaatca caaaatagaa gatcagatgt tcccatcaga 1620
 807 atccaaacga gaggaagatg aagaatattc ttgggattct gggagtctct ttgagagttc 1680
 808 tgcaaagact caagtgtgta tacctgagtc tatgtatcag aaagtaatgg agataaatag 1740
 809 agaagtagaa gagcttctct agaagccatc tgccttcaag cctgcccgtg aaatgcaaaa 1800
 810 gactgttcca aataaagcct ttgaattgaa gaatgaacaa acattgagag cagctcagat 1860
 811 gttcccatca gaatccaaac aaaaggacga tgaagaaaat tcttgggatt ctgagagtcc 1920

42207 same errors
 42237 - Please insert to explain locations
 of NS/Xaas.

please see
 error summary
 sheet.

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 12/18/2003

PATENT APPLICATION: US/10/729,340

TIME: 08:56:41

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

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813 cgatacctta agtggaaaat tagaagagtc tcctgttaaa gatggtcttc tgaagcctac 2040
814 ctgtggaagg aaagtttctc ttccaaataa agccttagaa ttaaaggaca gagaaacatt 2100
815 caaagcagag tctcctgata aagatggtct tctgaagcct acctgtggaa ggaaagtctc 2160
816 tcttccaaat aaagccttag aattaaagga cagagaaaca ctcaaagcag agtctcctga 2220
817 taatgatggt cttctgaagc ctacctgtgg aaggaaagtt tctcttccaa ataaagcttt 2280
818 agaattgaag gacagagaaa cattcaaagc agctcagatg ttcccatcag aatccaaaca 2340
819 aaaggatgat gaagaaaatt cttgggattt tgagagtttc cttgagactc tcttacagaa 2400
820 tgatgtgtgt ttacccaagg ctacacatca aaaagaattc gataccttaa gtggaaaatt 2460
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831 ggaacttaaa aaagataact gtgaacaaat tacagcaaaa atggaacaaa tgaaaaataa 3120
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833 caaaaaagct aaatgggaac aagagctctg cagtgtgaga ttgcctttaa atcaagaaga 3240
834 agagaagaga agaaatgtcg atatattaaa agaaaaaatt agaccggaag agcaacttag 3300
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838 actgaaacat caacaccagg tgaaggaaaa taaatacttt gaggacatta agattttaca 3540
839 agaaaaagaat gctgaacttc aaatgaccct aaaactgaaa cagaaaacag taacaaaaag 3600
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1122 <210> SEQ ID NO: 32

1123 <211> LENGTH: 1397

1124 <212> TYPE: PRT

1125 <213> ORGANISM: Homo sapiens

W<

1126 <400> SEQUENCE: 32

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1130           20              25              30
1131 Ile Val His Ser Gly Asp Leu Arg Lys Ile His Lys Ala Ala Ser Arg
1132           35              40              45
1133 Gly Gln Val Arg Lys Leu Glu Lys Met Thr Lys Arg Lys Lys Thr Ile
1134           50              55              60
1135 Asn Leu Asn Ile Gln Asp Ala Gln Lys Arg Thr Ala Leu His Trp Ala
1136           65              70              75              80
1137 Cys Val Asn Gly His Glu Glu Val Val Thr Phe Leu Val Asp Arg Lys
1138           85              90              95
1139 Cys Gln Leu Asp Val Leu Asp Gly Glu His Arg Thr Pro Leu Met Lys
1140           100             105             110

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/729,340

DATE: 12/18/2003

TIME: 08:56:41

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

```

1141 Ala Leu Gln Cys His Gln Glu Ala Cys Ala Asn Ile Leu Ile Asp Ser
1142      115      120      125
1143 Gly Ala Asp Ile Asn Leu Val Asp Val Tyr Gly Asn Thr Ala Leu His
1144      130      135      140
1145 Tyr Ala Val Tyr Ser Glu Ile Leu Ser Val Val Ala Lys Leu Leu Ser
1146 145      150      155      160
1147 His Gly Ala Val Ile Glu Val His Asn Lys Ala Ser Leu Thr Pro Leu
1148      165      170      175
1149 Leu Leu Ser Ile Thr Lys Arg Ser Glu Gln Ile Val Glu Phe Leu Leu
1150      180      185      190
1151 Ile Lys Asn Ala Asn Ala Asn Ala Val Asn Lys Tyr Lys Cys Thr Ala
1152      195      200      205
1153 Leu Met Leu Ala Val Cys His Gly Ser Ser Glu Ile Val Gly Met Leu
1154 210      215      220
1155 Leu Gln Gln Asn Val Asp Val Phe Ala Ala Asp Ile Cys Gly Val Thr
1156 225      230      235      240
1157 Ala Glu His Tyr Ala Val Thr Cys Gly Phe His His Ile His Glu Gln
1158      245      250      255
1159 Ile Met Glu Tyr Ile Arg Lys Leu Ser Lys Asn His Gln Asn Thr Asn
1160      260      265      270
1161 Pro Glu Gly Thr Ser Ala Gly Thr Pro Asp Glu Ala Ala Pro Leu Ala
1162      275      280      285
1163 Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp
1164 290      295      300
1165 Glu Ala Ala Pro Leu Val Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu
1166 305      310      315      320
1167 Val Glu Lys Thr Pro Asp Glu Ala Ala Ser Leu Val Glu Gly Thr Ser
1168      325      330      335
1169 Asp Lys Ile Gln Cys Leu Glu Lys Ala Thr Ser Gly Lys Phe Glu Gln
1170      340      345      350
1171 Ser Ala Glu Glu Thr Pro Arg Glu Ile Thr Ser Pro Ala Lys Glu Thr
1172      355      360      365
1173 Ser Glu Lys Phe Thr Trp Pro Ala Lys Gly Arg Pro Arg Lys Ile Ala
1174 370      375      380
1175 Trp Glu Lys Lys Glu Asp Thr Pro Arg Glu Ile Met Ser Pro Ala Lys
1176 385      390      395      400
1177 Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys
1178      405      410      415
1179 Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala
1180      420      425      430
1181 Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys
1182      435      440      445
1183 Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn
1184 450      455      460
1185 Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr
1186 465      470      475      480
1187 Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val
1188      485      490      495
1189 Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu

```


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```

1190          500          505          510
1191 Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu
1192          515          520          525
1193 Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln
1194          530          535          540
1195 Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp
1196 545          550          555          560
1197 Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser
1198          565          570          575
1199 Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp
1200          580          585          590
1201 Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu
1202          595          600          605
1203 Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu
1204          610          615          620
1205 Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gly Lys Pro Ser
1206 625          630          635          640
1207 Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala
1208          645          650          655
1209 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro
1210          660          665          670
1211 Ser Glu Ser Lys Glu Lys Asp Tyr Glu Glu Asn Ser Trp Asp Thr Glu
1212          675          680          685
1213 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala
1214          690          695          700
1215 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser
1216 705          710          715          720
1217 Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser
1218          725          730          735
1219 Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala
1220          740          745          750
1221 Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln
1222          755          760          765
1223 Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu
1224          770          775          780
1225 Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu
1226 785          790          795          800
1227 Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys
1228          805          810          815
1229 Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp Lys Ile
1230          820          825          830
1231 Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ala
1232          835          840          845
1233 Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met
1234          850          855          860
1235 Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe
E--> 1236 865          870          (870)-875          880
1237 Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu
1238          885          890          895

```

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```

1239 Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu
1240          900          905          910
1241 Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
1242          915          920          925
1243 Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His
1244          930          935          940
1245 Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser
1246 945          950          955          960
1247 Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu
1248          965          970          975
1249 Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met
1250          980          985          990
1251 Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu
1252          995          1000          1005
1253 Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu
1254          1010          1015          1020
1255 Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn
1256 1025          1030          1035          1040
1257 Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu
1258          1045          1050          1055
1259 Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala
1260          1060          1065          1070
1261 Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn
1262          1075          1080          1085
1263 Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn
1264          1090          1095          1100
1265 Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr
1266 1105          1110          1115          1120
1267 Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile
1268          1125          1130          1135
1269 Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu
1270          1140          1145          1150
1271 Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu
1272          1155          1160          1165
1273 Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu
1274          1170          1175          1180
1275 Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro
1276 1185          1190          1195          1200
1277 Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg
1278          1205          1210          1215
1279 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln
1280          1220          1225          1230
1281 Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val
1282          1235          1240          1245
1283 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys
1284          1250          1255          1260
1285 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val
1286 1265          1270          1275          1280
1287 Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys

```

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1288		1285		1290		1295
1289	Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His					
1290		1300		1305		1310
1291	Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser					
1292		1315		1320		1325
1293	Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala					
1294		1330		1335		1340
1295	Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys					
1296	1345		1350		1355	1360
1297	Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr					
1298		1365		1370		1375
1299	Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala					
1300		1380		1385		1390
1301	Glu Thr Glu Asn Ser					
1302		1395				
1303	(25362054_1.DOC 23) <i>delete</i>					

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/729,340

DATE: 12/18/2003

TIME: 08:56:42

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:288 W: Application Number is Repeated, <150> PRIOR APPLICATION NUMBER
L:29 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180
L:65 M:283 W: Missing Blank Line separator, <400> field identifier
L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:212 M:283 W: Missing Blank Line separator, <400> field identifier
L:251 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8 ✓
L:251 M:283 W: Missing Blank Line separator, <400> field identifier ✓
L:263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8 ✓
L:263 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:8 ✓
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:660 ✓
L:271 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:283 W: Missing Blank Line separator, <400> field identifier
L:287 M:283 W: Missing Blank Line separator, <400> field identifier
L:295 M:283 W: Missing Blank Line separator, <400> field identifier
L:303 M:283 W: Missing Blank Line separator, <400> field identifier
L:311 M:283 W: Missing Blank Line separator, <400> field identifier
L:321 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15 ✓
L:321 M:283 W: Missing Blank Line separator, <400> field identifier ✓
L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15 ✓
L:349 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:15 ✓
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1620 ✓
M:341 Repeated in SeqNo=15
L:362 M:283 W: Missing Blank Line separator, <400> field identifier ✓
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16 ✓
L:426 M:252 E: No. of Seq. differs, <211> LENGTH:Input:513 Found:512 SEQ:16 ✓
L:433 M:283 W: Missing Blank Line separator, <400> field identifier
L:441 M:283 W: Missing Blank Line separator, <400> field identifier
L:449 M:283 W: Missing Blank Line separator, <400> field identifier
L:494 M:283 W: Missing Blank Line separator, <400> field identifier
L:502 M:283 W: Missing Blank Line separator, <400> field identifier
L:510 M:283 W: Missing Blank Line separator, <400> field identifier
L:586 M:283 W: Missing Blank Line separator, <400> field identifier
L:761 M:283 W: Missing Blank Line separator, <400> field identifier
L:769 M:283 W: Missing Blank Line separator, <400> field identifier
L:779 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26 ✓
L:779 M:283 W: Missing Blank Line separator, <400> field identifier ✓
L:787 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26 ✓
L:787 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26 ✓
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:420 ✓
M:341 Repeated in SeqNo=26

VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/729,340

TIME: 08:56:42

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12182003\J729340.raw

L:848 M:283 W: Missing Blank Line separator, <400> field identifier
L:983 M:283 W: Missing Blank Line separator, <400> field identifier
L:991 M:283 W: Missing Blank Line separator, <400> field identifier
L:999 M:283 W: Missing Blank Line separator, <400> field identifier
L:1014 M:283 W: Missing Blank Line separator, <400> field identifier
L:1126 M:283 W: Missing Blank Line separator, <400> field identifier
L:1236 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32 ✓